

FIG. 1

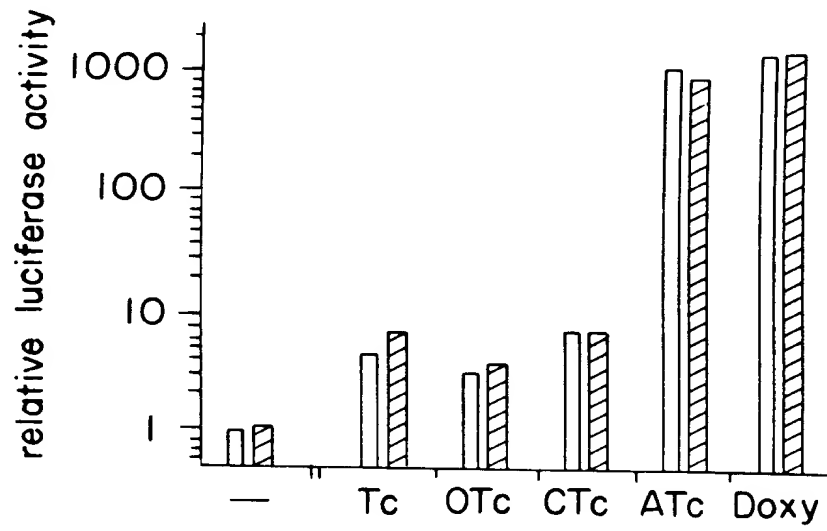


FIG.2

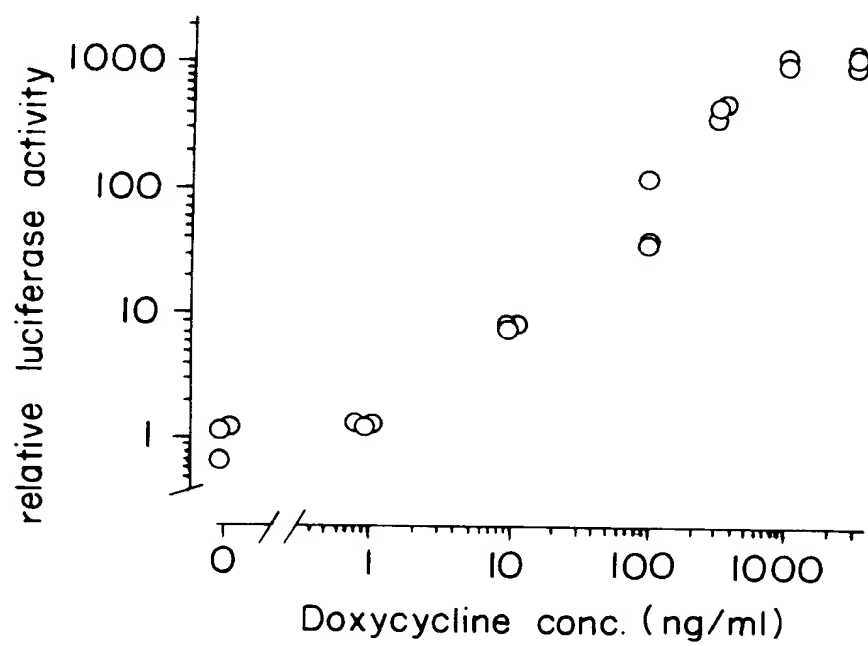


FIG. 3

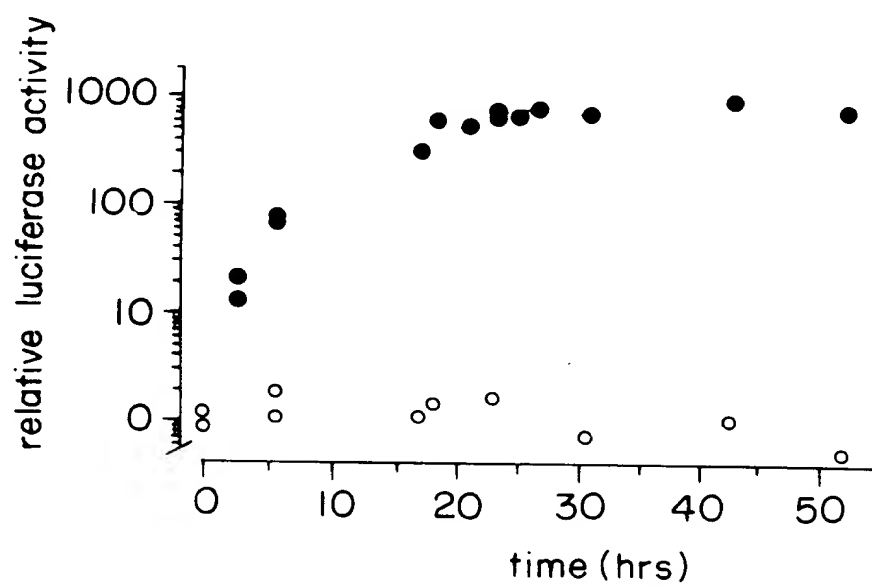
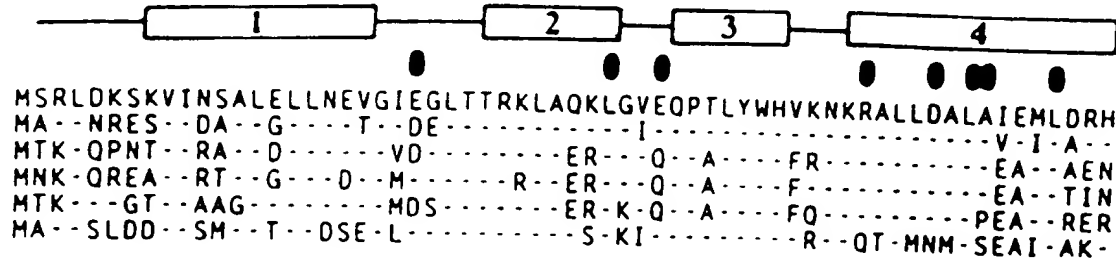
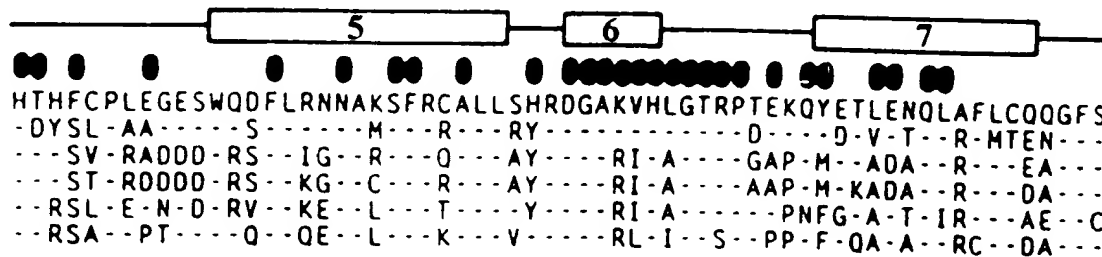


FIG. 4

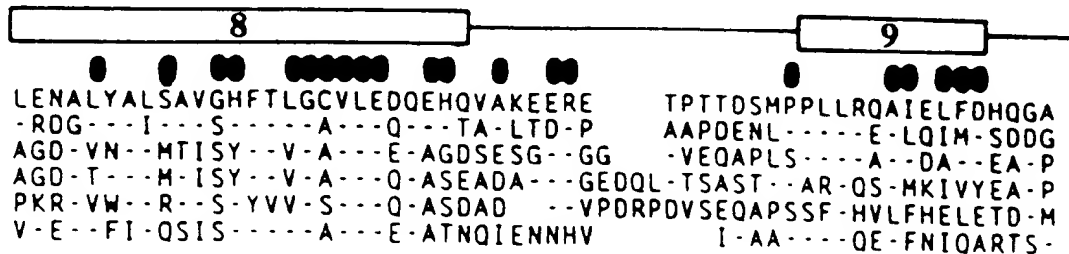
H T H



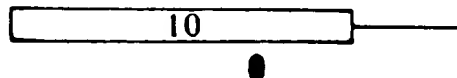
63 B
D
A
C
G
E



126 B
D
A
C
G
E



182 B
182 D
183 A
186 C
184 G
179 E



-Q---H---SL-R-F-V--TALLQIVGGOKLIIPFC
 DA--EQ--AV-VD--A-RRLVVRNVEGPRKGDD
 DA--ER--A---G---MRLTTNOIEVLKNVDE
 DA--N---DSL-A-F-RLRAAVLATD
 -M--H---KSL-F-FSA--DEKKHTPIEDGNK

207 B
218 C
216 A
219 C
210 G
211 E

FIG. 5

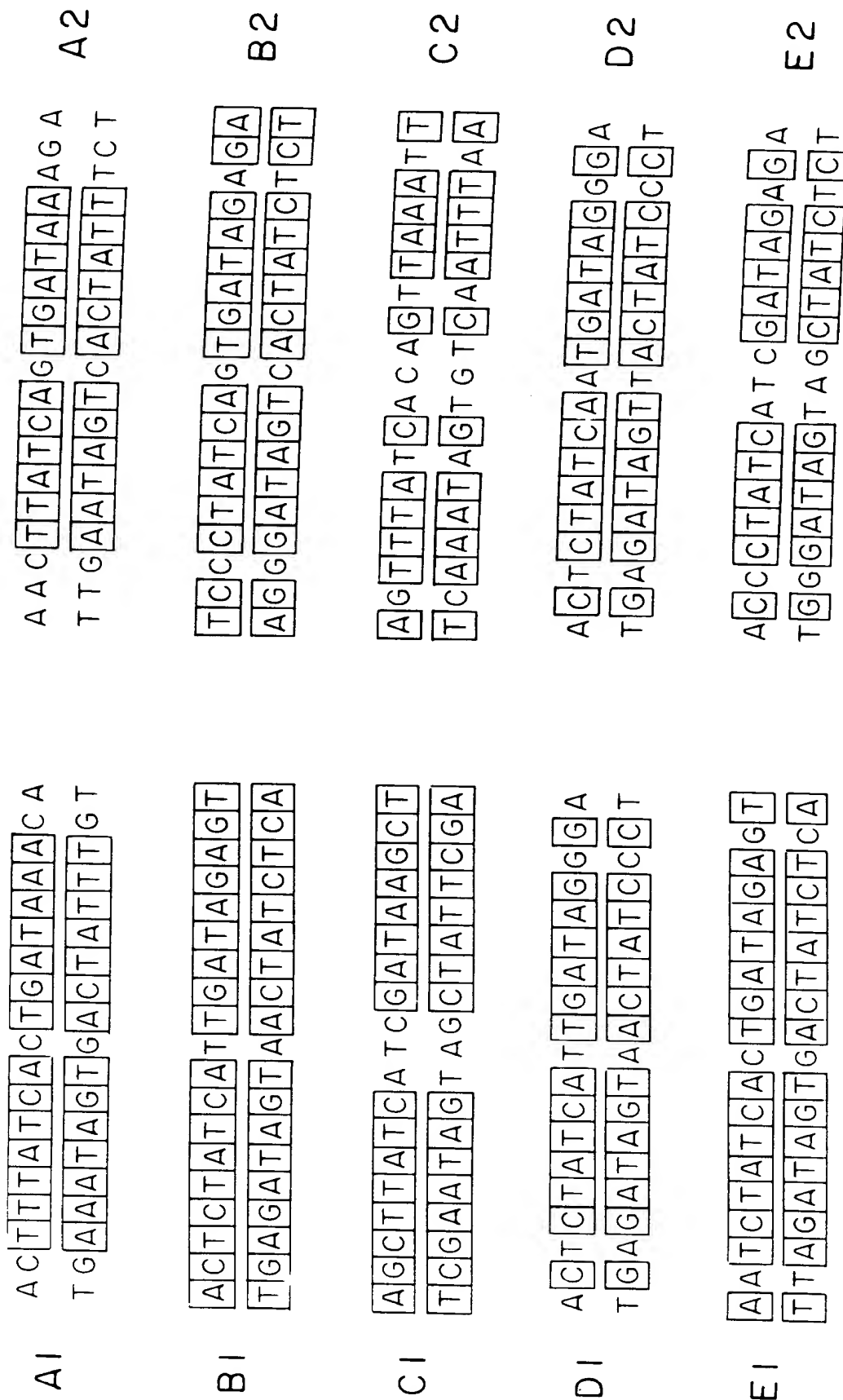


FIG. 6

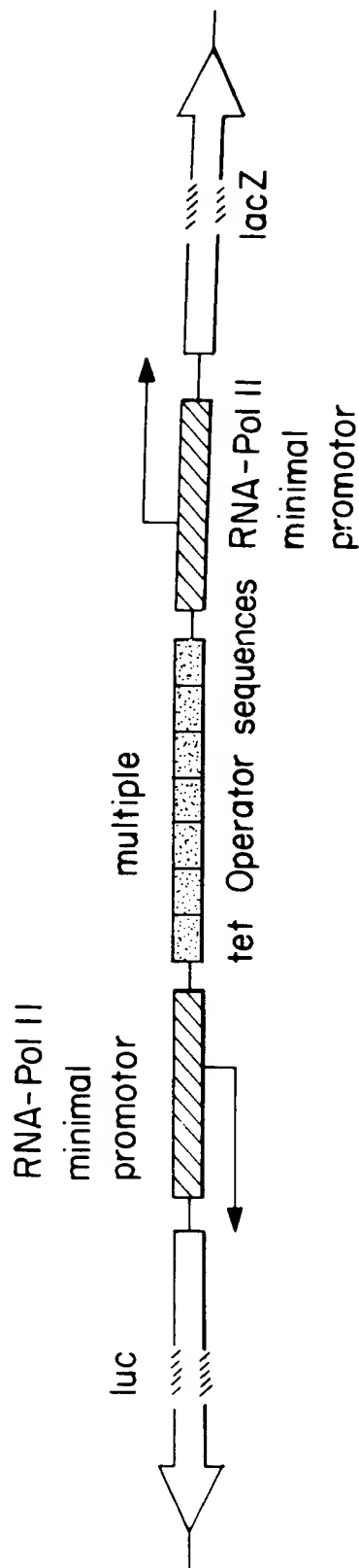


FIG. 7A

5' GAATTCGGGG
EcoRI + 75

CCGCGGAGGCTGGATCGGTCCCGGTGTCTTCTATGGAGGTCAAAACAGCGTGGA

+ 1
←
C

TGGCGTCTCCAGGCGATCTGACGGTTCCTAAACGAGCTCTGCTTATATAGG
P_{hCMV}*-3 -3;

tet O

TC (GAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTC)₇GAGC

TCGGTACCCGGGTCGAGTAGGCGTGTACGGTGGGAGGCCTATATAAGCAGAG
P_{hCMV}*-1
-53

CTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGA
+ 1 →

CCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCCCCGAATTC 3'
+ 75 EcoRI

FIG. 7B

5' ⁺¹⁹ AGATCT GCAGGGTCGC
Bgl II Pst I

⁺¹
←
A

TCGGTGTTCGAGGCCACACGCGTCACCTT AATATGCGAAGTGGACCGGATC
P_{K*} -37 -37

tet O
TC (GAGTTTACCACTCCCTATCAGTGATAGAGAAAAGTGAAAGTC)₇ GAGC
→ ←

TCGGTACCCGGGTCGAGTAGGCGTGTACGGTGGGAGGCCTATATAAGCAGAG
-53 P_{hCMV*} -1

CTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGCCATCCACGCTGTTTTGA
+1 →

CCTCCATAGAAGACACCGGGACCGATCCAGCCTCCGCGGCCCCGAAATTC 3'
+75 EcoRI

66000 24E 4260

FIG. 8A

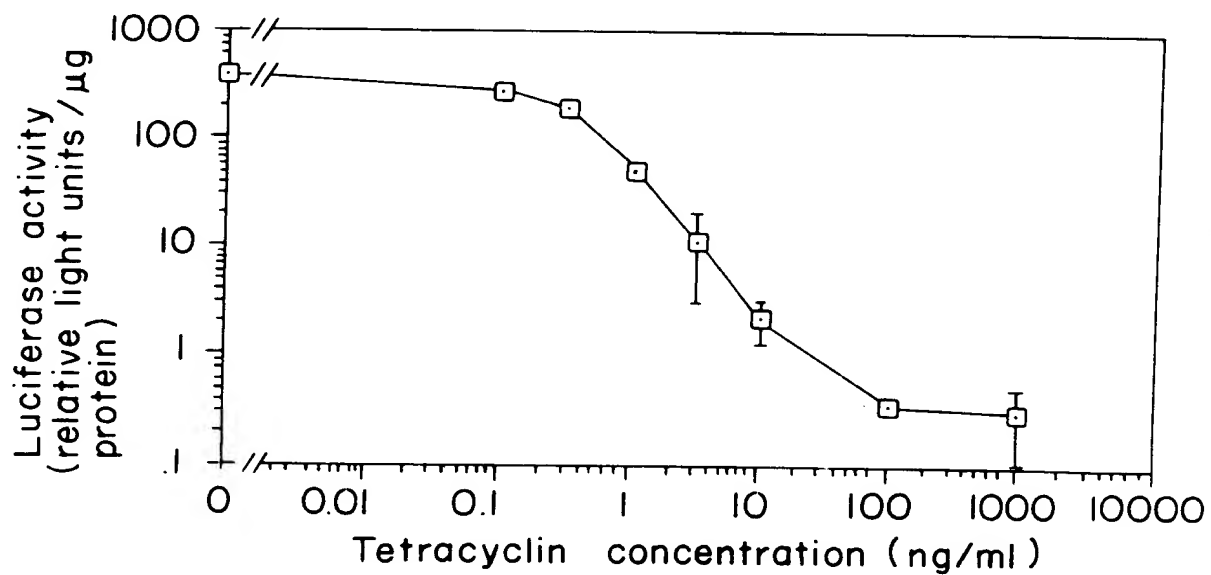


FIG. 8B

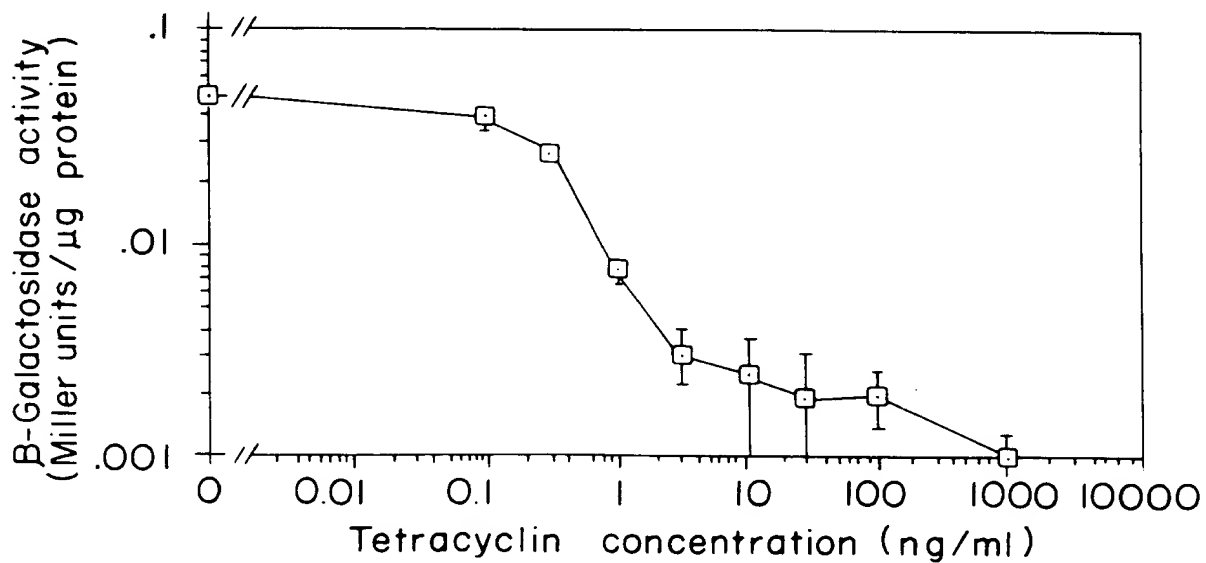


FIG. 9A

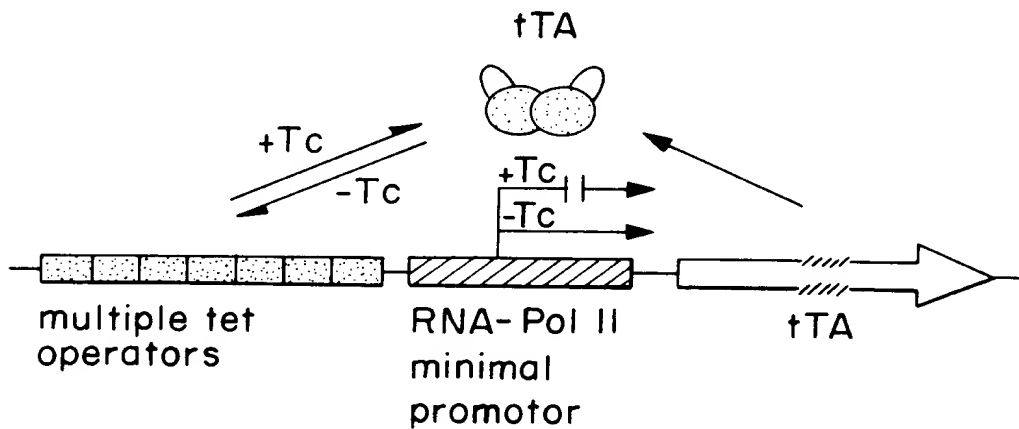


FIG. 9B

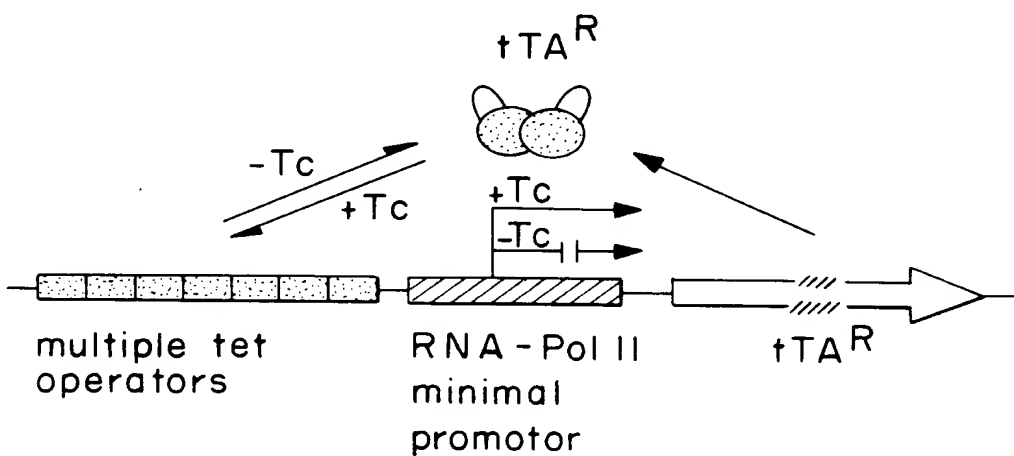


FIG. 10

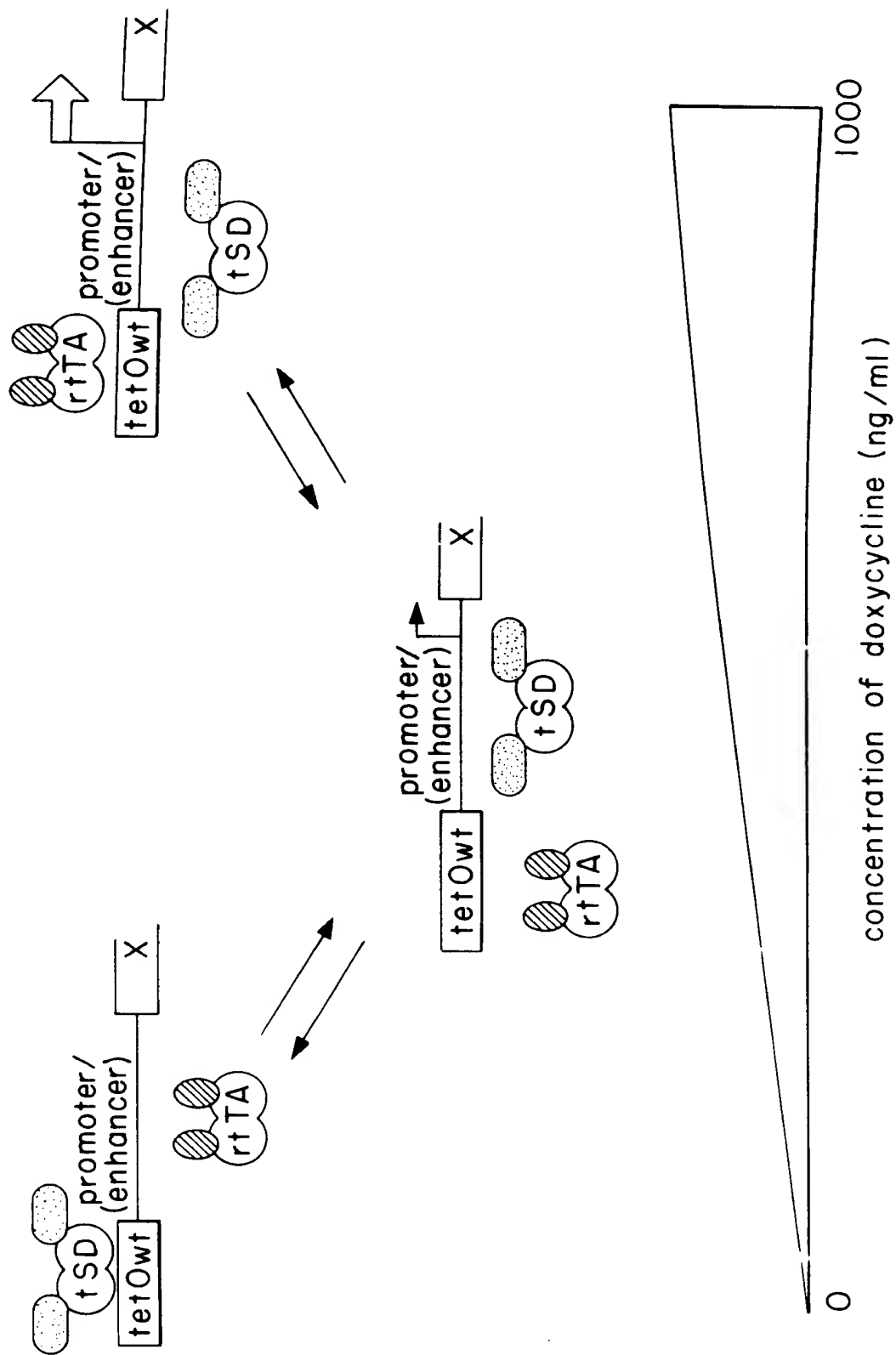


FIG. 11

pUHD141Kr-1

Pcmv →

pUHD141sma-1

ATG TCT... tetR gene ... TCC CCG GGT AAC TAAGTAAGGATCC — An —

in-frame fusion of the Krueppel repr./silencing domain

pUHD141erb-1

in-frame fusion of the v-erbA repr./silencing domain

FIG.12

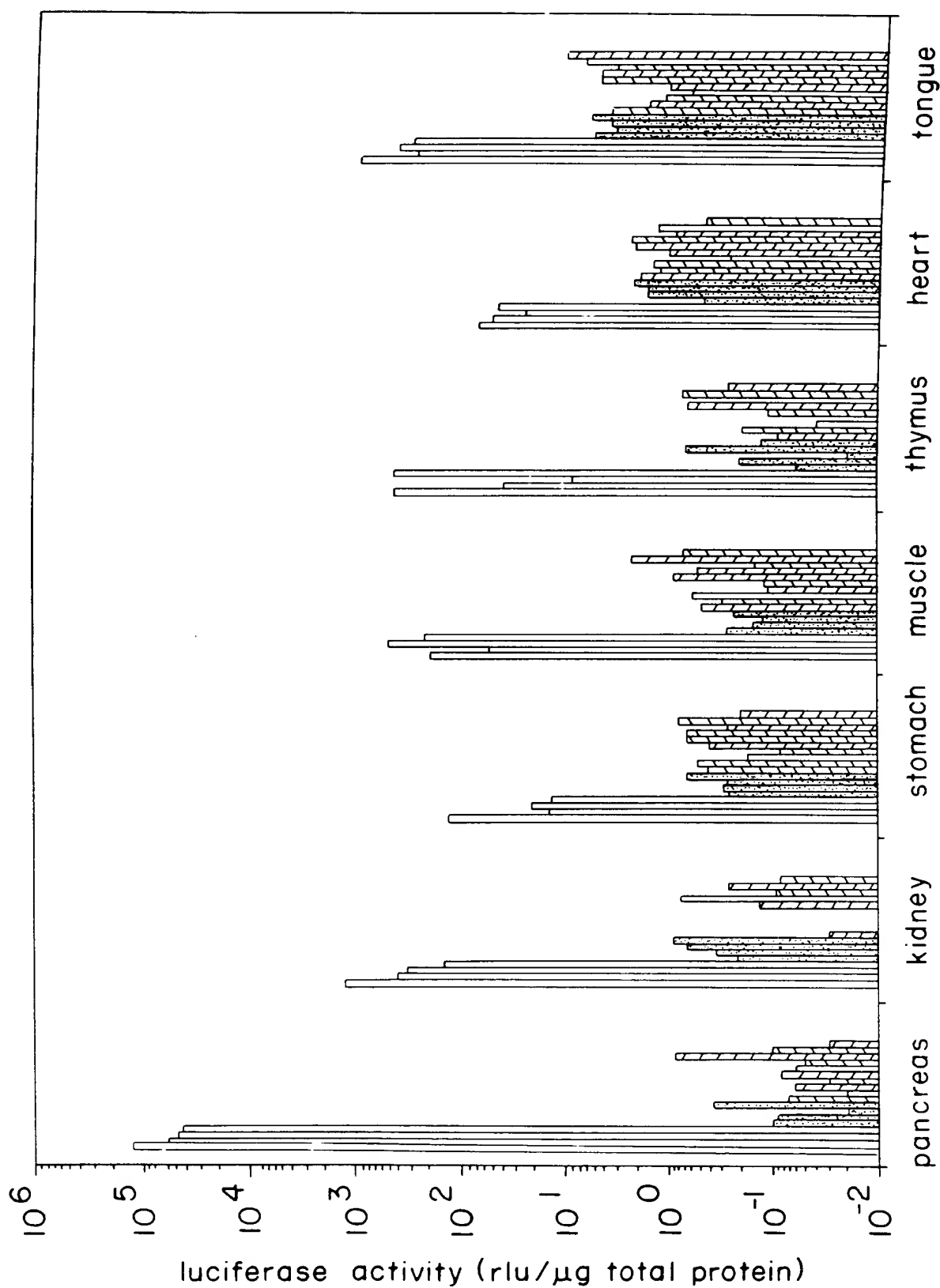


FIG. 13

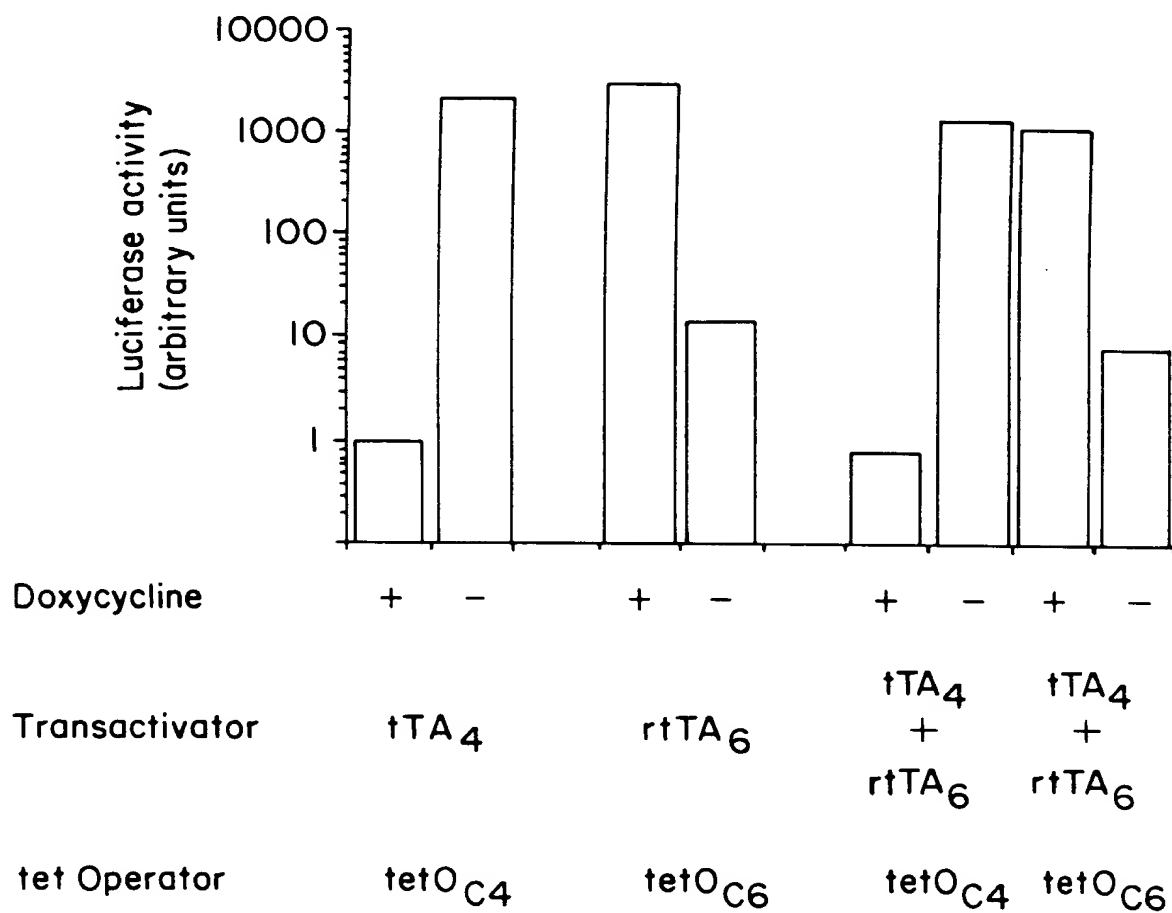


FIG.14A

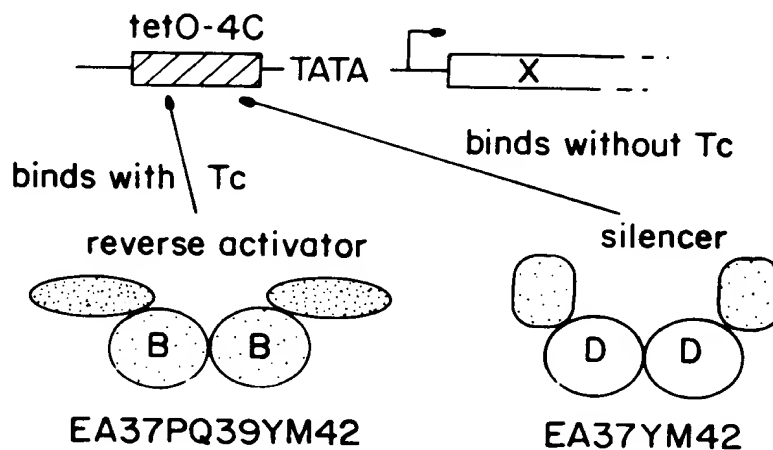


FIG.14B

